This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims:

Claims 1-21: Cancelled

22. (Currently Amended) A method for assaying an allele via hybridization, comprising:

hybridizing a target oligonucleotide to oligonucleotides that are coupled to different bead sets to form a complex, wherein the oligonucleotides that are coupled to different bead sets are oligonucleotides with and without a spacer wherein complementary regions of the oligonucleotides flank the spacer, further wherein the complementary regions of the oligonucleotides hybridize with a contiguous sequence on the target oligonucleotide to provide perfect sequence homology between the complementary regions of the oligonucleotide and the contiguous sequence of the target oligonucleotide; and

assaying the complex for specificity of different alleles.

23. (Previously Presented) The method of claim 22 further comprising separating allele specific nucleic acid fragments.

24. (Previously Presented) The method of claim 23 wherein separating allele specific nucleic acid fragments comprises using oligonucleotides for specific polymorphisms coupled to different bead sets.

25. (Previously Presented) The method of claim 22 further comprising coupling oligonucleotides for specific polymorphisms to different bead sets.

26. (Previously Presented) The method of claim 22 further comprising coupling oligonucleotides with and without a spacer to different bead sets.

27. (Previously Presented) The method of claim 22 further comprising obtaining a target nucleic acid sample containing multiple alleles, each allele having a unique set of heterosequence sites.

28. (Previously Presented) The method of claim 27 further comprising amplifying the target nucleic acid.

29. (Previously Presented) The method of claim 27 further comprising denaturing the target nucleic acid into single stranded nucleic acid.

30. (Previously Presented) The method of claim 22 further comprising confirming the sequence of the target oligonucleotide by hybridizing the target oligonucleotide with a second bead set that is complementary to the target oligonucleotide and measuring the hybridization by flow cytometry.

31. (Previously Presented) The method of claim 22 wherein the target oligonucleotide is an HLA allele.

32. (Previously Presented) The method of claim 22 wherein the bead sets that are coupled to the oligonucleotides with and without a spacer are conjugated with or attached to different oligonucleotides and can be identified by a fluorescence color ratio incorporated into one or more beads of the bead sets.

33. (Previously Presented) The method of claim 22 wherein the spacer is nucleic acid bases.

34. (Previously Presented) The method of claim 33 wherein the bases are random bases.

35. (Previously Presented) The method of claim 22 wherein the spacer is in the middle of the oligonucleotide sequence.

36. (Previously Presented) The method of claim 22 wherein the oligonucleotides that are coupled to different bead sets are selected to have perfect sequence homology to their respective target oligonucleotides.

37. (Previously Presented) The method of claim 22 wherein each different oligonucleotide for a specific allele is coupled to a different bead set.

38. (Previously Presented) The method of claim 22 wherein the different bead sets have one or more beads with different specific fluorescence color ratios.

39. (Previously Presented) The method of claim 22 wherein the beads are fluorescent beads.